

CLAIMS

1. A CGTase variant having an amino acid sequence which differs from the amino acid sequence of a parent CGTase, wherein the parent CGTase is a *Bacillus* CGTase and the difference between the amino acid sequence of the CGTase variant and the amino acid sequence of the parent CGTase comprises one or more of the following:

47C; 47D; 47E; 47F; 47G; 47I; 47K; 47N; 47P; 47R; 47S; 47T; 47V; 47W; 47Y; 145D; 145H; 145I; 145N; 145Q; 145V; 146H; 146K; 146L; 146T; 146V; 146Y; 147C; 147D; 147E; 147N; 147Q; 196C; 196E; 196F; 196G; 196H; 196I; 196K; 196L; 196M; 196P; 196Q; 196R; 196T; 196V; 196W; 196Y; 371C; 371E; 371F; 371H; 371I; 371K; 371L; 371M; 371Q; 371R; 371T; 371V; or 371W;

wherein each position corresponds to the position of the amino acid sequence of the mature CGTase obtained from *Bacillus circulans* strain 251.

2. The CGTase variant of claim 1, wherein the difference comprises one or more of the following: 47C; 47D; 47E; 47F; 47G; 47I; 47K; 47N; 47P; 47R; 47S; 47T; 47V; 47W; or 47Y.

3. The CGTase variant of claim 1, wherein the difference comprises one or more of the following: 145D; 145H; 145I; 145N; 145Q; or 145V.

4. The CGTase variant of claim 1, wherein the difference comprises one or more of the following: 146H; 146K; 146L; 146T; 146V; or 146Y.

5. The CGTase variant of claim 1, wherein the difference comprises one or more of the following: 147C; 147D; 147E; 147N; or 147Q.

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6. The CGTase variant of claim 1, wherein the difference comprises one or more of the following: 196C; 196E; 196F; 196G; 196H; 196I; 196K; 196L; 196M; 196P; 196Q; 196R; 196T; 196V; 196W; or 196Y.

7. The CGTase variant of claim 1, wherein the difference comprises one or more of the following: 371C; 371E; 371F; 371H; 371I; 371K; 371L; 371M; 371Q; 371R; 371T; 371V; or 371W.

8. The CGTase variant of claim 1, wherein the difference comprises:

47K/145E/146V/147N;
 47K/145E/146E/147N;
 47K/145D/146R/147D;
 47K/145D/146E/147D;
 47K/145E/146V/147N/196H;
 47K/145E/146E/147N/196H;
 47K/145E/146V/147N/196H/371R;
 47K/145E/146E/147N/196H/371R;
 47K/145D/146R/147D/196H;
 47K/145D/146E/147D/196H;
 47K/145D/146R/147D/196H/371R;
 47K/145D/146R/147D/196H/371R;
 47K/196H;
 47R/196H;
 145E/146V/147N;
 145E/146E/147N;
 145D/146R/147D;
 145D/146E/147D;
 47K/371R; or
 47R/371R.

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9. The CGTase variant of claim 1, wherein the difference comprises:

R47K/S145E/S146V/D147N;

R47K/S145E/S146E/D147N;

5 R47K/S145D/S146R;

R47K/S145D/S146E;

R47K/S145E/S146V/D147N/D196H;

R47K/S145E/S146E/D147N/D196H;

R47K/S145E/S146V/D147N/D196H/D371R;

10 R47K/S145E/S146E/D147N/D196H/D371R;

R47K/S145D/S146R/D196H;

R47K/S145D/S146E/D196H;

R47K/S145D/S146R/D196H/D371R;

R47K/S145D/S146R/D196H/D371R.

15 R47K/D196H;

S145E/S146V/D147N;

S145E/S146E/D147N;

S145D/S146R;

S145D/S146E; or

R47K/D371R.

20 10. The CGTase variant of claim 1, wherein the difference comprises:

S145E/E146V/T147N;

S145E/T147N;

25 S145D/E146R/T147D;

S145D/T147D;

S145E/E146V/T147N/D196H;

S145E/T147N/D196H;

S145E/E146V/T147N/D196H/D371R;

30 S145E/T147N/D196H/D371R;

S145D/E146R/T147D/D196H;

S145D/T147D/D196H;

S145D/E146R/T147D/D196H/D371R;

S145D/E146R/T147D/D196H/D371R;
 S145E/E146V/T147N;
 S145E/T147N;
 S145D/E146R/T147D;
 5 S145D/T147D;
 K47R/D371R; or
 K47R/D196H.

11. The CGTase variant of claim 1, wherein the parent CGTase is derived from a *Bacillus* selected from the group consisting of
 10 *Bacillus autolyticus*, *Bacillus cereus*, *Bacillus circulans*,
Bacillus circulans var. *alkalophilus*, *Bacillus coagulans*, *Bacillus firmus*, a strain of *Bacillus halophilus*, *Bacillus macerans*,
Bacillus megaterium, *Bacillus ohbensis*, *Bacillus*
stearothermophilus, *Bacillus subtilis*.

12. The CGTase variant of claim 1, wherein the parent CGTase is derived from a *Bacillus* selected from the group consisting of
 15 *Bacillus* sp. Strain 1011, *Bacillus* sp. Strain 38-2, *Bacillus* sp.
 Strain 17-1, *Bacillus* sp. 1-1, *Bacillus* sp. Strain B1018, *Bacillus*
 20 *circulans* Strain 8, or *Bacillus circulans* Strain 251, or a mutant
 or a variant thereof.

13. The CGTase variant according to claim 1, wherein the parent CGTase is derived from *Bacillus circulans* Strain 251, or a mutant
 25 of a variant thereof.

14. A method of producing cyclodextrin, comprising treating a starch with a CGTase variant of claim 1.

30 15. The method of claim 14, wherein the cyclodextrin is an α -cyclodextrin.

16. The method of claim 14, wherein the cyclodextrin is a β -cyclodextran.

5 17. The method of claim 14, wherein the cyclodextrin is a γ -cyclodextrin.

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